

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 3, 2005, 23:17:42 ; Search time 101 Seconds
(without alignments)
3127.531 Million cell updates/sec

Title: US-10-071-838-2

Perfect score: 2983

Sequence: 1 MDVVEVAGSWWAQEREDIM.....TSGPCLCGHLESSQPPPGF 549

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 02:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2983	100.0	549	1	TBC3 HUMAN
2	2971	99.6	549	2	Q61PX1
3	2971	99.6	549	2	AAH71680
4	2945	98.7	549	2	Q6DHYS
5	2188.5	73.4	1406	1	UBP6 HUMAN
6	1544.5	51.8	376	2	Q15635
7	1479	49.6	346	2	Q6PD72
8	1479	49.6	346	2	AAH58890
9	1477.5	49.5	376	2	Q6PJJ2
10	1477.5	49.5	376	2	AAH33670
11	1346	45.1	291	2	Q6DCB4
12	655	22.0	819	1	US6L MOUSE
13	655	22.0	841	2	BAC97847
14	651	21.8	828	1	US6L HUMAN
15	651	21.8	838	2	BAA02807
16	603.5	20.2	250	2	Q6CUD7
17	602	20.2	224	2	Q8NCR5
18	576	19.3	1085	2	Q9U2D8
19	576	19.3	1085	2	CAB60374
20	574.5	19.3	1021	2	Q7K711
21	574.5	19.3	1021	2	CAB45741
22	530	17.8	391	2	Q7QFV5
23	500.5	16.8	498	2	Q7PPV8
24	455	15.3	457	2	Q18357
25	455	15.3	485	2	Q95RE0
26	455	15.3	571	2	Q7KR75
27	323.5	10.8	356	2	Q81347
28	321.5	10.8	537	2	Q8BHL3
29	321.5	10.8	537	2	Q91XR3
30	321.5	10.8	655	2	Q6GQW9
31	320.5	10.7	533	2	Q9H8Z2

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32	320.5	10.7	584	2	Q6IN54	Q6IN54 homo sapien
33	320.5	10.7	584	2	AAH72453	Aah72453 homo sapi
34	320.5	10.7	622	2	Q6P530	Q6P530 homo sapien
35	320.5	10.7	622	2	AAH63112	Aah63112 homo sapi
36	319	10.7	353	2	Q8LAF3	Q8Laf3 arabidopsis
37	317.5	10.6	304	2	Q9M894	Q9m894 arabidopsis
38	306.5	10.3	532	2	Q9Y1V8	Q9y1v8 halocynthia
39	305.5	10.2	500	1	TB10 MOUSE	P58802 mus musculu
40	302	10.1	298	2	Q8L756	Q8l756 arabidopsis
41	301	10.1	446	2	Q8IV04	Q8iv04 homo sapien
42	301	10.1	446	2	AAH62999	Aah62999 homo sapi
43	301	10.1	450	2	AAH36873	Aah36873 homo sapi
44	300	10.1	500	2	Q8CI62	Q8ci62 mus musculu
45	299.5	10.0	508	1	TB10_HUMAN	Q9bxi6 homo sapien

ALIGNMENTS

RESULT 1
TBC3_HUMAN STANDARD; PRT; 549 AA.
AC Q8IZP1; Q9H0B9; Q9UDD4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE TBC1 domain family member 3 (Rab GTPase-activating protein PRCL17)
DE (Prostate cancer gene 17 protein) (TRE17 alpha protein).
GN Name=TBC1D3; Synonyms=PRCL17;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, AND DISEASE.
RX MEDLINE=22246263; PubMed=12359748;
RA Pei L., Peng Y., Yang Y., Ling X.B., Van Eynhoven W.G., Nguyen K.C.,
RA Rubin M., Hoey T., Powers S., Li J.,
RT "PRCL17, a novel oncogene encoding a Rab GTPase-activating protein, is
RT amplified in prostate cancer."
RL Cancer Res. 62:5420-5424(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=21154917; PubMed=11230166; DOI=10.1101/gr.154701;
RA Wiemann S., Weil B., Wellenreuther R., Gassnerhuber J., Glassl S.,
RA Ansgorge W., Boecker M., Bloeker H., Bauersachs S., Blum H.,
RA Lauber J., Duesterhoeft A., Beyer A., Koehrer K., Strack N.,
RA Mewes H.-W., Ottenwaelder B., Obermaier B., Tampe J., Heubner D.,
RA Wambutt R., Korn B., Klein M., Poustka A.,
RT "Towards a catalog of human genes and proteins: sequencing and
RT analysis of 500 novel complete protein coding human cDNAs."
RL Genome Res. 11:422-435(2001).
RN [3]
RP SEQUENCE OF 1-52 FROM N.A.
RX MEDLINE=93228825; PubMed=8471161;
RA Onno M., Nakamura T., Mariage-Samson R., Hillova J., Hill M.,
RT "Human TRB17 oncogene is generated from a family of homologous
RT polymorphic sequences by single-base changes."
RL DNA Cell Biol. 12:107-118(1993).
RN [4]
RP SEQUENCE OF 1-52 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94010310; PubMed=8406013;
RA Onno M., Nakamura T., Hillova J., Hill M.,
RT "Identification of novel sequences in the repertoire of hypervariable
RT TRB17 genes from immortalized nonmalignant and malignant human
RT keratinocytes."
RL Gene 131:209-215(1993).
RN [5]
RP TISSUE SPECIFICITY.
RX MEDLINE=22506395; PubMed=12604796; DOI=10.1073/pnas.0437015100;
RA Paulding C.A., Ruvoilo M., Haber D.A.,

Appendix 1, page

RT "The Tre2 (USP6) oncogene is a hominoid-specific gene."
RL Proc. Natl. Acad. Sci. U.S.A. 100:2507-2511(2003).
CC -1- FUNCTION: Acts as a GTPase activating protein for RAB5. Does not
CC act on RAB4 or RAB11.
CC -1- TISSUE SPECIFICITY: Expressed in liver, skeletal muscle, kidney,
CC pancreas, spleen, testis, ovary, small intestine and peripheral
CC blood leukocytes. Overexpressed in prostate cancers.
CC -1- DISEASE: May be involved in forms of prostate cancers.
CC -1- SIMILARITY: Contains 1 Rab-GAP TBC domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF540953; AAN33117.1; -.
DR EMBL; AL136860; CAB66794.1; -.
DR EMBL; X71377; CAB94197.1; -.
DR Genew; HGNC:19031; TBCID3.
DR MIM; 607741; -.
DR InterPro; IPR000195; RabGAP_TBC.
DR Pfam; PF00566; TBC; 1.
DR SMART; SM00164; TBC; 1.
DR PROSITE; PS50086; TBC_RABGAP; 1.
KM GTPase activation; Proto-oncogene.
FT DOMAIN 101 293 Rab-GAP TBC.
FT CONFLICT 117 117 I -> T (in Ref. 2).
FT CONFLICT 137 137 R -> K (in Ref. 2).
FT CONFLICT 354 354 Q -> K (in Ref. 2).
FT CONFLICT 526 526 P -> Q (in Ref. 2).
SQ SEQUENCE 549 AA; 62168 MW; 831DA747D0B6F400 CRC64;

Query Match 100.0%; Score 2983; DB 1; Length 549;
Best Local Similarity 100.0%; Pred. No. 1.4e-179;
Matches 549; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDVEVAGSWMWAQEREDIMKYEGHAGLPEDKGPFRSYNNVNDHIGIVHETELPPL 60
DB 1 MDVEVAGSWMWAQEREDIMKYEGHAGLPEDKGPFRSYNNVNDHIGIVHETELPPL 60

QY 61 TAREAKQIRREISRSKSKWVMDLGWEKYSRKLDIDRAYKGMNIRGPMWSVLNIEEM 120
DB 61 TAREAKQIRREISRSKSKWVMDLGWEKYSRKLDIDRAYKGMNIRGPMWSVLNIEEM 120

QY 121 KLNKPGRYQIMKEKGRSSEHIQIRIDRVSGTLRKHIFPRDRYGTQKRELLHLLAYEEY 180
DB 121 KLNKPGRYQIMKEKGRSSEHIQIRIDRVSGTLRKHIFPRDRYGTQKRELLHLLAYEEY 180

QY 181 NPEVGYCRDLISHIALFLYLPEEDAFWALVOLLAERHSLQGFHSPNGTVOGLQDQOE 240
DB 181 NPEVGYCRDLISHIALFLYLPEEDAFWALVOLLAERHSLQGFHSPNGTVOGLQDQOE 240

QY 241 HVVATSQPKTMGHQDKDLCGQCSPLGCLIRILIDGISLGLTLRLMDVYLIVEGEQALMPI 300
DB 241 HVVATSQPKTMGHQDKDLCGQCSPLGCLIRILIDGISLGLTLRLMDVYLIVEGEQALMPI 300

QY 301 TRIAFKVOQKRLTKTSRCGFWARFCNRFVDTWARDEDTVLKHLRASMKKLTRKQGLDLP 360
DB 301 TRIAFKVOQKRLTKTSRCGFWARFCNRFVDTWARDEDTVLKHLRASMKKLTRKQGLDLP 360

QY 361 AKPEQSSASRPVPASRGKTLCKGDRQAPPGPARFPRPIWSASPPRARSSTPCPGA 420
DB 361 AKPEQSSASRPVPASRGKTLCKGDRQAPPGPARFPRPIWSASPPRARSSTPCPGA 420

QY 421 VREDTYPVGTQGVSPPALAOGPGQSWRFLQWNSMPRLPTDLVGEPMFRHYDFRQSCWV 480
DB 421 VREDTYPVGTQGVSPPALAOGPGQSWRFLQWNSMPRLPTDLVGEPMFRHYDFRQSCWV 480

QY 481 RAISQEDQLAPCWAQEAHPAERVRSAPAPSTDSQGTFFRARDQPCAPTSGPCLGHL 540
DB 481 RAISQEDQLAPCWAQEAHPAERVRSAPAPSTDSQGTFFRARDQPCAPTSGPCLGHL 540

DB 481 RAISQEDQLAPCWAQEAHPAERVRSAPAPSTDSQGTFFRARDQPCAPTSGPCLGHL 540
QY 541 ESSQFPFPGF 549
DB 541 ESSQFPFPGF 549

RESULT 2
Q6IPX1 PRELIMINARY; PRT; 549 AA.
ID Q6IPX1
AC Q6IPX1;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE TBC1 domain family, member 3.
GN Name=TBCID3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedlin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grumwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalek U., Smallus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071680; AAH71680.1; -.
DR InterPro; IPR000195; RabGAP_TBC.
DR Pfam; PF00566; TBC; 1.
DR SMART; SM00164; TBC; 1.
DR PROSITE; PS50086; TBC_RABGAP; 1.
SQ SEQUENCE 549 AA; 62231 MW; 5657E5602B3655F5 CRC64;

Query Match 99.6%; Score 2971; DB 2; Length 549;
Best Local Similarity 99.5%; Pred. No. 8.2e-179;
Matches 546; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MDVEVAGSWMWAQEREDIMKYEGHAGLPEDKGPFRSYNNVNDHIGIVHETELPPL 60
DB 1 MDVEVAGSWMWAQEREDIMKYEGHAGLPEDKGPFRSYNNVNDHIGIVHETELPPL 60

QY 61 TAREAKQIRREISRSKSKWVMDLGWEKYSRKLDIDRAYKGMNIRGPMWSVLNIEEM 120
DB 61 TAREAKQIRREISRSKSKWVMDLGWEKYSRKLDIDRAYKGMNIRGPMWSVLNIEEM 120

QY 121 KLNKPGRYQIMKEKGRSSEHIQIRIDRVSGTLRKHIFPRDRYGTQKRELLHLLAYEEY 180
DB 121 KLNKPGRYQIMKEKGRSSEHIQIRIDRVSGTLRKHIFPRDRYGTQKRELLHLLAYEEY 180

QY 181 NPEVGYCRDLISHIALFLYLPEEDAFWALVOLLAERHSLQGFHSPNGTVOGLQDQOE 240
DB 181 NPEVGYCRDLISHIALFLYLPEEDAFWALVOLLAERHSLQGFHSPNGTVOGLQDQOE 240